

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2002, 12:33:38 ; Search time 21.5 Seconds
(without alignments)
4820.544 Million cell updates/sec

Title: US-10-025-514-16
Perfect score: 2675
Sequence: 1 MEDPQGAACKTDTSHHQD.....RDLKCCMGCKSCVSPVKA 503

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2027	75.8	418	4 Q96ES1	Q96es1 homo sapien
2	2026	75.7	418	4 Q96BF9	Q96bf9 homo sapien
3	1908	71.3	396	6 O00394	O00394 cercopithec
4	1470	55.0	413	11 O54761	O54761 spermophilu
5	1462.5	54.7	421	6 O46519	O46519 equus caball
6	1446.5	54.1	413	11 P97277	P97277 mesocricetu
7	1374	51.4	406	11 Q84118	Q84118 meriones un
8	1342	50.2	413	6 Q28665	Q28665 oryctolagus
9	1340	50.1	413	11 Q9VC20	Q9vc20 mus musculu
10	1334	49.9	410	11 Q91WH5	Q91wh5 mus musculu
11	1334	49.9	413	11 Q91XB8	Q91xb8 mus musculu
12	1334	49.9	413	11 Q91V74	Q91v74 mus musculu
13	1330	49.7	425	11 Q91XC1	Q91xc1 mus musculu
14	1325	49.5	413	6 Q07298	Q07298 oryctolagus
15	1324	49.5	413	11 Q8VC41	Q8vc41 mus musculu
16	1323	49.5	456	6 O62663	O62663 oryctolagus

17	1310	49.0	413	11 Q63969	Q63969 mus saxicol
18	1307	48.9	413	6 Q28666	Q28666 oryctolagus
19	1290	48.2	413	11 O54762	O54762 spermophilu
20	1184	44.3	413	11 Q91X22	Q91x22 mus musculu
21	1026	38.4	433	13 Q9YIB8	Q9yib8 xenopus lae
22	1010	37.8	197	4 Q13747	Q13747 homo sapien
23	849.5	31.8	420	11 Q60552	Q60552 mesocricetu
24	849	31.7	407	4 Q9UNU9	Q9unu9 homo sapien
25	845	31.6	410	13 Q90323	Q90323 cyprinus ca
26	829	31.0	418	11 Q91X80	Q91x80 mus musculu
27	828	31.0	418	11 Q8VCH3	Q8vch3 mus musculu
28	825	30.8	418	11 Q91W80	Q91w80 mus musculu
29	820.5	30.7	415	6 Q9GMA6	Q9gma6 sus scrofa
30	818	30.6	418	11 Q03734	Q03734 mus musculu
31	816	30.5	427	4 Q96B25	Q96bz5 homo sapien
32	812	30.4	418	11 Q62257	Q62257 mus musculu
33	811.5	30.3	418	11 Q91WP6	Q91wp6 mus musculu
34	810.5	30.3	418	11 Q62258	Q62258 mus musculu
35	794	29.7	404	6 Q9N212	Q9n212 bos taurus
36	765.5	28.7	406	11 Q88292	Q88292 rattus norv
37	760	28.4	406	6 Q9GK37	Q9gk37 sus scrofa
38	758	28.3	411	11 Q8R421	Q8r421 rattus norv
39	757.5	28.3	415	6 Q27984	Q27984 bos taurus
40	745.5	27.9	418	11 Q9D7D2	Q9d7d2 mus musculu
41	742	27.7	412	11 Q63556	Q63556 rattus norv
42	725	27.1	413	11 Q9CQ32	Q9cq32 mus musculu
43	722.5	27.0	397	11 Q91WQ0	Q91wq0 mus musculu
44	714	26.7	423	11 P97569	P97569 rattus norv
45	673	25.2	371	6 Q9TTE1	Q9tte1 bos taurus

ALIGNMENTS

RESULT 1

Q96ES1 ID Q96ES1 PRELIMINARY; PRT; 418 AA.
AC Q96ES1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1.
DE Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011991; AAH11991.1;
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 418 AA; 46722 MW; 70165484573B7F16 CRC64;

Query Match 75.8%; Score 2027; DB 4; Length 418;
Best Local Similarity 99.7%; Pred. No. 4.6e-130;
Matches 393; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	2	EDPQGAACKTDTSHHQDHPFNKTPNLAFAFSLYRQLAHQSNSTNFIFFSPVSIATA 61	
Db	25	EDPQGAACKTDTSHHQDHPFNKTPNLAFAFSLYRQLAHQSNSTNFIFFSPVSIATA 84	
QY	62	FAMLSLGTADTHDELEGNLNLTEIPQAQIHEGFOELLRTLNQPSOLOLTGTGNGLFL 121	
Db	85	FAMLSLGTADTHDELEGNLNLTEIPQAQIHEGFOELLRTLNQPSOLOLTGTGNGLFL 144	
QY	122	SEGLKLVDFLEEDVKLYHSEAFVNFQGTTERAKKQINDYVEKGTQGVKIVDLVKELDRDT 181	

Db 145 SGLKLVDFKLEDDVKKLHSEAFVNGDTEAAKKQINDVEGTQGIIVDLVKELDRDT 204
 QY 182 VFALVNYIFFKQKWERPEVVDTEEDFHVDDQVTVKVPMMKRLGMFNIOHCKKLSWVL 241
 Db 205 VFALVNYIFFKQKWERPEVVDTEEDFHVDDQVTVKVPMMKRLGMFNIOHCKKLSWVL 264
 QY 242 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 301
 Db 265 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324
 QY 302 SVLGQGLGTTKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLEAIPMSI 361
 Db 325 SVLGQGLGTTKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLEAIPMSI 384
 QY 362 PPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPOTK 395
 Db 385 PPEVKFNKPFVFLMIDQNTKSPFLMGKVVNPOTK 418
 RESULT 2
 Q96BF9 PRELIMINARY; PRT; 418 AA.
 ID Q96BF9
 AC Q96BF9
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1
 antitrypsin, member 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; BC015642; AAH15642.1; -.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
 KW Serpin.
 SQ SEQUENCE 418 AA; 46708 MW; FF0E525F303542AE CRC64;
 Query Match 75.7%; Score 2026; DB 4; Length 418;
 Best Local Similarity 99.7%; Pred. No. 5.3e-130;
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EDPOGDAQKTDTSHTDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIAT 61
 Db 25 EDPOGDAQKTDTSHTDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIAT 84
 QY 62 FAMILSLGTADTHDEILEGLNLFNLTEIPEAQIHEGFQELLRTINOPDSQLOLTGNGFL 121
 Db 85 FAMILSLGTADTHDEILEGLNLFNLTEIPEAQIHEGFQELLRTINOPDSQLOLTGNGFL 144
 QY 122 SEGKLVDFKLEDDVKKLYHSEAFVNGDTEAAKKQINDVEGTQGIIVDLVKELDRDT 181
 Db 145 SEGKLVDFKLEDDVKKLYHSEAFVNGDTEAAKKQINDVEGTQGIIVDLVKELDRDT 204
 QY 182 VFALVNYIFFKQKWERPEVVDTEEDFHVDDQVTVKVPMMKRLGMFNIOHCKKLSWVL 241
 Db 205 VFALVNYIFFKQKWERPEVVDTEEDFHVDDQVTVKVPMMKRLGMFNIOHCKKLSWVL 264
 QY 242 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 301
 Db 265 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324
 QY 302 SVLGQGLGTTKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLEAIPMSI 361
 Db 325 SVLGQGLGTTKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLEAIPMSI 384

QY 362 PPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPOTK 395
 Db 385 PPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPOTK 418
 RESULT 3
 Q00394 PRELIMINARY; PRT; 396 AA.
 ID Q00394
 AC Q00394
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Alpha-1-antitrypsin (Fragment).
 GN PI.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Sinohara H.;
 RT "Cloning and sequencing of complementary DNAs encoding alpha-2-HS
 glycoprotein, alpha-1-antitrypsin, and beta-actin from african green
 monkey, Cercopithecus aethiops."
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=85026667; PubMed=6333329;
 RA Colau B., Chuchana P., Bollen A.;
 RT "Revised sequence of full-length complementary DNA coding for human
 alpha 1-antitrypsin."
 RL DNA 3:327-330(1984).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AB004044; BAA20264.1; -.
 DR HSSP; P01009; 9API.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin.
 FT NON_TER 1 1
 SQ SEQUENCE 396 AA; 44587 MW; 1042EABFAA0A2825 CRC64;
 Query Match 71.3%; Score 1908; DB 6; Length 396;
 Best Local Similarity 92.9%; Pred. No. 5.4e-122;
 Matches 367; Conservative 19; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MEDPOGDAQKTDTSHTDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIAT 60
 Db 2 VEDPOGDAQKTDTSHTDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIAT 61
 QY 61 AFAMLSLGTADTHDEILEGLNLFNLTEIPEAQIHEGFQELLRTINOPDSQLOLTGNGFL 120
 Db 62 AFAMLSLGTADTHDEILEGLNLFNLTEIPEAQIHEGFQELLRTINOPDSQLOLTGNGFL 121
 QY 121 LSEGLKLVDFKLEDDVKKLYHSEAFVNGDTEAAKKQINDVEGTQGIIVDLVKELDRDT 180
 Db 122 LNSKSVVDKLEDDVKKLYHSEAFVNGDTEAAKKQINDVEGTQGIIVDLVKELDRDT 181
 QY 181 TVFALVNYIFFKQKWERPEVVDTEEDFHVDDQVTVKVPMMKRLGMFNIOHCKKLSWVL 240
 Db 182 TVFALVNYIFFKQKWERPEVVDTEEDFHVDDQVTVKVPMMKRLGMFNIOHCKKLSWVL 241
 QY 241 LLMKYLGNATAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 300
 Db 242 LLMKYLGNATAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 301
 QY 301 KSVLGQGLGTTKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLEAIPMSI 360
 Db 325 SVLGQGLGTTKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLEAIPMSI 384

```

Db 302 KTVLGHGKITKVFNSGADLSGVTEDAPLKLKAVHKAVLTIDEKGTAAAGAMFLEAIPNS 361
QY 361 IPEVKFNKPFVFLMTEQNTKSPLEMGKVNPQK 395
Db 362 IPEVKFNKPFVFLMTEQNTKSPLEMGKVNPQK 396

RESULT 4
O54761
ID O54761 PRELIMINARY; PRT; 413 AA.
AC O54761;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-antitrypsin-like protein.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scluridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alphas-antitrypsin-like genes in hibernating
RT species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB000550; BAA24420.1; -.
DR HSSP; P01009; IOLP.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 413 AA; 45953 MW; B08D2544695EE0F4 CRC64;

Query Match 55.0%; Score 1470; DB 11; Length 413;
Best Local Similarity 71.9%; Pred. No. 3.8e-92;
Matches 277; Conservative 54; Mismatches 54; Indels 0; Gaps 0;

QY 9 AOKTDTSHHDDHPTFNKIPNLAEAFSLYRQLAHQSNSTNFIFFSPVSTATAFAMLSLG 68
Db 27 AQETGASKHDOEHPASHRIAPNLAEAFSLYRVLAHESNTNFIFFSPVSTATAMALASLSLG 86
QY 69 TKADTHDEILGLNFNLTEPEAOIHGEGFQELRLTLNOPSQQLTGTGNGLFSEGLKV 128
Db 87 TKADTHQIMEGLGNLTETAESDIHQGFQHLQLTLNKPNSQLTGTGNGLFIDHNLKLL 146
QY 129 DKFLEDVKLYHSEAFVTFNGDTEEAQKQINDYVEKGTQKIVDLVKELDRDTVFLVNY 188
Db 147 DKFLQDVKNLYHSEAFSTDFNTTEEAQKQINTYVEKGTQKIVDLVKELDRDVSFLVNY 206
QY 189 IFFGKWERPEVKDTEEDFHVQVTVTVKPMKRLGMFNIHQCKLSSWLIMKYLGN 248
Db 207 IFFGKWERPEVKDTEEDFHVQVTVTVKPMKRLGMFNIHQCKLSSWLIMKYLGN 266
QY 249 ATAFELPDECKLQHLNELTHDIITKFLNEEDRRSASLHLPKLSITGTVDLKSVLGQLG 308
Db 267 ATAFELPDECKLQHLNELTHDIITKFLNEEDRRSASLHLPKLSITGTVDLKSVLGQLG 326
QY 309 ITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLEAIPNSIPPEVKEN 368
Db 327 ITNVSFKADLSGTTEDPLRVSQLHKAHLTIDERGTEAAGATFLEMPSPPEVKED 386
QY 369 KPFVFLMTEQNTKSPLEMGKVNPQK 393
Db 387 KPLWIIHSTKSPLEMGKVNPQK 411

RESULT 5

```

```

O46519
ID O46519 PRELIMINARY; PRT; 421 AA.
AC O46519;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antitrypsin.
GN SPI2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ARABIAN BREED;
RA Giffard J.M., Irvin Z.V., Bell T.K., Brandon R.B.;
RT "Equine alpha-1-antitrypsin gene.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF034077; AAC83412.1; -.
DR HSSP; P01009; 1KCT.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 421 AA; 46942 MW; D79B101312AC8259 CRC64;

Query Match 54.7%; Score 1462.5; DB 6; Length 421;
Best Local Similarity 70.0%; Pred. No. 1.3e-91;
Matches 278; Conservative 53; Mismatches 63; Indels 3; Gaps 1;

QY 2 EDPOGAAKTDTSHHDDH---PTFNKIPNLAEAFSLYRQLAHQSNSTNFIFFSPVSI 58
Db 25 EDLQGCVAQVQETHATAHDEEHLQEPAEHKTAPNLADFAFSLYRHVAHQSNNTNFIFFSPVSI 84
QY 59 ATAFAMLSLGTKADTHDEILGLNFNLTEPEAOIHGEGFQELRLTLNOPSQQLTGTGNG 118
Db 85 ATAFALLSLGAKGDTHTQILEGLSFLNTELAEAQIHGEGFQHLNLAHSDNQLTGTGNG 144
QY 119 LFLSEGLKLVKDFLEDVKLYHSEAFVTFNGDTEEAQKQINDYVEKGTQKIVDLVKELD 178
Db 145 LFLDESAKLLDKFLEDVKLYHSEAFVTFNGDTEEAQKQINDYVEKGTQKIVDLVKELD 204
QY 179 RDTFVFLVNYIFPKGKWERPEVKDTEEDFHVQVTVTVKPMKRLGMFNIHQCKLSS 238
Db 205 KDTVLALVNYIEFKGTWEPPEPEYTTQDFHVDKTTVTRVPMHRLSSFDVQYSDTLSS 264
QY 239 WVLLMKYLGNAATAFELPDECKLQHLNELTHDIITKFLNEEDRRSASLHLPKLSITGY 298
Db 265 WVLLLDYAGNATAFFLDPQGLQHLDELTKGILARFLGNRHSSFVNVVHLPKLSISGY 324
QY 299 DLKSVLGQLGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLEAIP 358
Db 325 DLTSILPELGITKVFNSROADLSGITEEVEPLTVSKALHKAHLTIDEKGTAAAGTTHWEIMP 384
QY 359 MSIPPEVKENKPFVFLMTEQNTKSPLEMGKVNPQK 395
Db 385 ISLPPDLKFNRPFLVIIDYDRNTKSPLEMGKVNPQK 421

RESULT 6
P97277
ID P97277 PRELIMINARY; PRT; 413 AA.
AC P97277;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antitrypsinase precursor.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.

```

RT	and implications for molecular evolution.";	
J.	Biochem. 116:582-588(1994).	
CCC	- - SIMILARITY: BELONGS TO THE SERPIN FAMILY.	
DRR	EMBL; S77822; AAB33367.1; -.	
DRR	HSSP; P01009; IOLP.	
DRR	InterPro: IPR000215; Serpin.	
DRR	Pfam; PF00079; serpin; 1.	
DRR	SMART; SM00093; SERPIN; 1.	
DRR	Serpin.	
DRR	SEQUENCE 406 AA; 45126 MW; 814613E44C7AA469 CRC64;	
DRR	Query Match 51.4%; Score 1374; DB 11; Length 406;	
DRR	Best Local Similarity 68.7%; Pred. No. 1.3e-85;	
DRR	Matches 265; Conservative 56; Mismatches 59; Indels 6; * Gaps	
QY	9 AOKTDTSHDDQHTFKNKTIPLNAEFAFSILYRQLAHQSNSTNIFFSPVSIATAFAMLSLG 68	:
DB	27 AEKTDSSH--QDH---IMASNLADPAFGLYRVLSHQSNNTNIFLSPLSIATALAMLSLG 80	:
QY	69 TKADPHDSEILSGLFNFTETPEAQIHGCFQBELRLTNPPDSQLOLTGTGCLFSLSEGLKLV 12	: :
DB	81 SKDDTKAQLLQGLHFNLTETSEADIHKGFOHLLKTLNRPDNEQLQTLTGSLSFVNNSLNV 14	: :
QY	129 DKFLEDVKLLYHSEAFVNGDTEEAKKOINDYVEKGTQGIYVDLVKELDRDTVFALVNY 18	: :
DB	141 ERFLEEVKNHHYHSEAFFVNFADSEAAKTLNSFEKATHGKIYVDLVKDELIDTVLALVNY 20	: :
QY	189 IFFKGKWPPEFVKDTEEDPHVDQVTVKVPMMKRLGMFNIHQCKKLSWLLMKYLG 24	: :
DB	201 IFFRGKWKPEPDPELTEADPHVDKSTTVKVPMMNRMGDFDVHCDTLLSWLLMDYLG 26	: :
QY	249 ATAIFFLDEKQHLNELTHDIIITKPLENEDRRSASLHLPKLSITGIYDLKSVLGQLG 30	: :
DB	261 ATAIFLLDEGKMOHLEQTLTKHEIYKFLQNRHRTSRANVHLPKLSISGTYNLKKVLSPLG 32	: :
QY	309 ITKVFNSGADISGVTEEAAPKLKSAVHKAVLTIDEKTEAAGAMFLEAIPMSIPPVEKFN 36	: :
DB	321 ITQVFNSGADUSGITTDVPLKLSKAVHKAVLTIDERTEAAGITVLEAVPMISPPDVCFK 38	: :
QY	369 KPFEFLIMEQNTKSPLEMGKVVNPQTQ 394	:
DB	381 NPFVVIICDKHQSPLEFVGKVVNPQTQ 406	:
RESULT 8		
Q28665	PRELIMINARY; PRT; 413 AA.	
IC	Q28665	
AD	Q28665;	
DT	01-NOV-1996 (TremBLrel. 01, Created)	
DT	01-NOV-1996 (TremBLrel. 01, Last sequence update)	
DT	01-DEC-2001 (TremBLrel. 19, Last annotation update)	
DE	Alpha-1-antiproteinase E precursor.	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Leporidae; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lacomorpha; Geniata; Leporidae; Oryctolagus	

OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC	NCBI_TaxID=9986;
CC	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=95251597; PubMed=7733871;
RA	Saito A., Shinohara H.;
RX	"Rabbit alpha-1-antiproteinase E: a novel recombinant serpin which
RT	does not inhibit proteinases.";
RT	Biochem. J. 307:369-375(1995).
RL	-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC	EMBL; D17725; BAA04579.1; -.
DR	HSP; P01009; 8API.
DR	InterPro; IPR000215; Serpin.
DR	Pfam; PF00079; serpin; 1.
DR	SMART; SM00093; SERPIN; 1.
DR	PROSITE; PS00284; SERPIN; 1.
KW	Serpin; Signal.
KW	POTENTIAL.
FT	SIGNAL 1 23
FT	CHAIN 24 413
FT	ALPHA-1-ANTIPROTEINASE E.


```

QY 250 TAIFLPDEGKLOHLENLTHDITTFLENERDRSASLHLPKLSITGTYDLKSVLGQGI 309
Db 264 TAVFLLPDGGMQHLQTLSEKLSKFLNRRRLAQIHFPRLSISGEYNLKLMSPLGI 323
QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEGKTEAAGAMFLAIPMSIPPEVKFN 368
Db 324 TRIFNNGADLSGITEENAPLKSQAVHKAVLTIDETGTEAAAVTVLLAVPYSMPPIILRD 383
QY 369 KPFVFLMEQNTKSPFLMGKVVNPTOK 395
Db 384 HPFLFIIFEHTQSPFLVGKVDPTHK 410

RESULT 11
QY1XB8 PRELIMINARY; PRT; 413 AA.
AC QY1XB8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Similar to serine protease inhibitor 1-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011041; AAH11041.1; -.
DR EMBL; BC009818; AAH09818.1; -.
DR EMBL; BC010984; AAH10984.1; -.
DR EMBL; BC021780; AAH21780.1; -.
DR EMBL; BC021325; AAH21325.1; -.
DR EMBL; BC024108; AAH24108.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Protease; Serpin.
SQ SEQUENCE 413 AA; 45966 MW; 1AFDA1B0C96DFDCC CRC64;

Query Match 49.9%; Score 1334; DB 11; Length 413;
Best Local Similarity 64.3%; Pred. No. 7e-83;
Matches 249; Conservative 70; Mismatches 66; Indels 2; Gaps 2;

```

```

QY 10 QKTDTSHHDDHPTNKITPNLAFAFSLYRQLAHQSNTNFIFFSPVSIATAFAMLSLGT 69
Db 28 QETDTSQKDOQ-PASHEIATNLGDFALSLYRELHVQSNTNFIFFSPVSIATAFAMLSLGS 86
QY 70 KADTHDEILEGLNLFNLTEIPEAQIHEGFOELLRTLNQPDLSQQLTGTGNGFLSEGLKLV 129
Db 87 KGDTHQIILEGLQFNLTQTSADIHKSFOHLQTLNRPDSELQSLSTGNGFLVNDKLV 146
QY 130 KFLEDVKLYHSEAFVTFNGDTEEAQKQINDYVEKGTQGIQVLDVLEKELDRDTVFALVNYI 189
Db 147 KFLEAKNHQAEVFSVNFPAESEAKKVINDFVEKGTQGIQVLEKELDRDTVFALVNYI 206
QY 190 FFKGWERPFEVKDTEEDFHVQDVTTVKPMKRLGFMNIQCHKLSWSVLLMKYLGN 249
Db 207 LFKGKWKPKFPDENTEEAEFHVDESTTVKPMMTLSGMLDVHHCSTLSWSVLLMDYAGNA 266
QY 250 TAIFLPDEGKLOHLENLTHDITTFLENERDRSASLHLPKLSITGTYDLKSVLGQGI 309
Db 267 TAVFLLPDGGMQHLQTLSEKLSKFLNRRRLAQIHFPRLSISGEYNLKLMSPLGI 326
QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEGKTEAAGAMFLAIPMSIPPEVKFN 368
Db 327 TRIFNNGADLSGITEENAPLKSQAVHKAVLTIDETGTEAAAVTVLLQWPMSPPIILRD 386
QY 369 KPFVFLMEQNTKSPFLMGKVVNPTOK 395
Db 387 HPFLFIIFEHTQSPFLVGKVDPTHK 413

```

RESULT 12
QY1V74

```

ID QY1V74 PRELIMINARY; PRT; 413 AA.
AC QY1V74;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Unknown (Protein for MGC:13995) (Similar to serine protease inhibitor 1-3) (Protein for MGC:13994) (Hypothetical 46.0 kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011041; AAH11041.1; -.
DR EMBL; BC009818; AAH09818.1; -.
DR EMBL; BC010984; AAH10984.1; -.
DR EMBL; BC021780; AAH21780.1; -.
DR EMBL; BC021325; AAH21325.1; -.
DR EMBL; BC024108; AAH24108.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Hypothetical protein; Protease; Serpin.
SQ SEQUENCE 413 AA; 45951 MW; 89FA3BF10ABC1B8 CRC64;

Query Match 49.9%; Score 1334; DB 11; Length 413;
Best Local Similarity 64.9%; Pred. No. 7e-83;
Matches 251; Conservative 68; Mismatches 66; Indels 2; Gaps 2;

```

```

QY 10 QKTDTSHHDDHPTNKITPNLAFAFSLYRQLAHQSNTNFIFFSPVSIATAFAMLSLGT 69
Db 28 QETDTSQKDOQ-PASHEIATNLGDFALSLYRELHVQSNTNFIFFSPVSIATAFAMLSLGS 86
QY 70 KADTHDEILEGLNLFNLTEIPEAQIHEGFOELLRTLNQPDLSQQLTGTGNGFLSEGLKLV 129
Db 87 KGDTHQIILEGLQFNLTQTSADIHKSFOHLQTLNRPDSELQSLSTGNGFLVNDKLV 146
QY 130 KFLEDVKLYHSEAFVTFNGDTEEAQKQINDYVEKGTQGIQVLDVLEKELDRDTVFALVNYI 189
Db 147 KFLEAKNHQAEVFSVNFPAESEAKKVINDFVEKGTQGIQVLEKELDRDTVFALVNYI 206
QY 190 FFKGWERPFEVKDTEEDFHVQDVTTVKPMKRLGFMNIQCHKLSWSVLLMKYLGN 249
Db 207 LFKGKWKPKFPDENTEEAEFHVDESTTVKPMMTLSGMLDVHHCSTLSWSVLLMDYAGNA 266
QY 250 TAIFLPDEGKLOHLENLTHDITTFLENERDRSASLHLPKLSITGTYDLKSVLGQGI 309
Db 267 TAVFLLPDGGMQHLQTLSEKLSKFLNRRRLAQIHFPRLSISGEYNLKLMSPLGI 326
QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEGKTEAAGAMFLAIPMSIPPEVKFN 368
Db 327 TRIFNNGADLSGITEENAPLKSQAVHKAVLTIDETGTEAAAVTVLLAVPYSMPPIILRD 386
QY 369 KPFVFLMEQNTKSPFLMGKVVNPTOK 395
Db 387 HPFLFIIFEHTQSPFLVGKVDPTHK 413

```

RESULT 13
QY1XC1


```
ID Q91XC1 PRELIMINARY; PRT; 425 AA.
AC Q91XC1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:4210562) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC010988; AAH10988.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
FT NON_TER
SQ SEQUENCE 425 AA; 47157 MW; EA9E50E40C33CAFC CRC64;

Query Match 49.7%; Score 1330; DB 11; Length 425;
Best Local Similarity 64.6%; Pred. No. 1.4e-82;
Matches 250; Conservative 68; Mismatches 67; Indels 2; Gaps 2;

QY 10 QKTDTSDDHPTFNKTPNLAFAFSLYROLAHQSNSTNIFSPVSIATAFAMLSIGT 69
Db 40 QETDTSQKQDS-PASHEIATNLGDFSAISLYRELHVQSNSTNIFSPVSIATAFAMLSIGS 98

QY 70 KADTHDEILGLNLFNLTEPEAQIHEGFQELLRLNQPSQLQTLTGNGFLSEGLK 129
Db 99 KGDTHQIILEGQFNLQTFSEADIIKSFQHLQTLNRPDSELSQLSTGNGFLVNNDLK 158

QY 130 KFEVDKVKLYHSEAFVNFQDTEEAQKQINDYVEKGTGQKIVDLVKELDRDRTVFALVNI 189
Db 159 KLEEAKNHYQAEVSVNFAESEAQKVINDEVEKGTGQKTAQAVKLLDQDTVFALANI 218

QY 190 FPKGKWERPEVVKDTEEDFHVDQVTVKVPMMKRLGMFNTOHCKLSWLLMKYLQNA 249
Db 219 LFKGKWKPKFPDENTEAEAFHVDSTTVKVPMMTLGMDLVHHCSTLSSWLLMDYAGNA 278

QY 250 TAIFFLPDEGKLOHLENLTHDIITKFLNEDRRSASLHLPKLSITCTYDLKSVLGQ 309
Db 279 TAVELPDGKMQHLEQLTSKELISKFLNRRRLAQIHFPRLSISGBYNLKTLMSP 338

QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGTAAAGAMFLEAIPMSIPPEVKFN 368
Db 339 TRIFNNGADLSGITENAPLKLSQAVHKAVLTIDETGTEAAATVLLAVPYSMPPILRFD 398

QY 369 KPFVFLMIDQNTKSPFLMGKVVNPTOK 395
Db 399 HPFLFIPEHTQSPFLGVGVVDPTHK 425

RESULT 14
Q07298
ID Q07298 PRELIMINARY; PRT; 413 AA.
AC Q07298;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antiprotease S-1 precursor.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93293795; PubMed=8514734;
RA Saito A., Sinohara H.;
```

```
RT "Rabbit plasma alpha-1-antiprotease S-1: cloning, sequencing,
RT expressionand, and proteinase inhibitory properties of recombinant
RT protein.";
RL J. Biochem. 113:456-461(1993).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; D16104; BAA03678.1; -.
DR HSP; P01009; BAPI.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 413 ALPHA-1-ANTIPROTEINASE S-1.
SQ SEQUENCE 413 AA; 45749 MW; 75C6004D6C7190BA CRC64;

Query Match 49.5%; Score 1325; DB 6; Length 413;
Best Local Similarity 65.2%; Pred. No. 2.9e-82;
Matches 253; Conservative 58; Mismatches 77; Indels 0; Gaps 0;

QY 7 DAAQKTDTSDDHPTFNKTPNLAFAFSLYROLAHQSNSTNIFSPVSIATAFAMLS 66
Db 25 DEAQETAVSSHEQDHPACHRIAPSLAEFALSLYREVAHESNTNIFSPVSIATAFAMLS 84

QY 67 LGTKADTHDEILGLNLFNLTEPEAQIHEGFQELLRLNQPSQLQTLTGNGFLSEGLK 126
Db 85 LGAKGDTHQVLEGLKFNLTAEAQIHDGFRHLLHTVNRPDSELSQLAAGNALVWHENLK 144

QY 127 LVDFKEDVKKLYHSEAFVNFQDTEEAQKQINDYVEKGTGQKIVDLVKELDRDRTVFALV 186
Db 145 LQHKFLEDAKNLXQSEAFVDFRDPQQAQKINSHEKGTGKIVDLVQLDARTLLALV 204

QY 187 NYIFFKQKWERPEVVKDTEEDFHVDQVTVKVPMMKRLGMFNTOHCKLSWLLMKYL 246
Db 205 NYVFFKQKWEKPEPENTKEEDFHVDATTVPVPMMSRLGMVYKFGHSTLASTVLRMDYK 264

QY 247 GNATFELPDGKLOHLENLTHDIITKFLNEDRRSASLHLPKLSITCTYDLKSVLGQ 306
Db 265 GNATALLPDPDEGKLOHLEDLTELAKFLAKSSFSRVVRFPKLSISTGYDLKPLGK 324

QY 307 LGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTAAAGAMFLEAIPMSIPPEVK 366
Db 325 LGITQVFSNADLSGITQEPEPLKVSQALHKAVLTIDERGTEAAGATEVGIMPSLPSVI 384

QY 367 FPKGKWERPEVVKDTEEDFHVDQVTVKVPMMKVVNPTQ 394
Db 385 FDRPFLFVIYSHELKSPFLGVGVVDPTQ 412

RESULT 15
Q8VC41
ID Q8VC41 PRELIMINARY; PRT; 413 AA.
AC Q8VC41;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to serine protease inhibitor 1-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021850; AAH21850.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 413 AA; 45995 MW; C96A4EC0A7951872 CRC64;
```

